Identifying novel biomarkers of IPF

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Background

- There is limited research conducted on idiopathic pulmonary fibrosis, and its pathogenesis is largely unknown so far. So far, IPF is only detected when symptoms (dry cough, chronic shortness of breath) set in, at which point the usual prognosis is death within 2-3 years. IPF is a rare disease that affects construction workers and smokers more than others.
- As such, the first step to unraveling the pathways behind IPF is to identify the biomarkers (genomic and proteomic signals that are upregulated or overexpressed) in IPF.
- The goal of this research is to identify and confirm the genomic upregulation of certain factors in IPF tissue.
- Building confidence in the link between protein regulation pathways and incidence of disease allows for the development of targeted therapeutic treatment.
- The long term goals for this project is the development of point of care technology that allows both the noninvasive treatment for IPF and individualized health care.

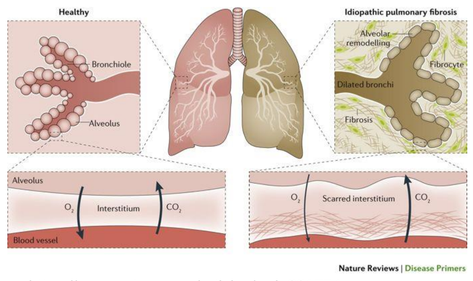
Results

Since the first approach took a bulk of the time in the summer, actual results have not been produced yet. Microarray data from GEO have been accessed and some analysis has been done, but meta-analysis is not complete yet. The next steps are to compare the expression profiles of lung tissues from multiple studies, and select the genes that have been reported as upregulated. Then, using IPF mouse lung tissue, I will perform immunohistochemistry for the most upregulated genes in order to confirm the expression profile provided by the GEO raw data.

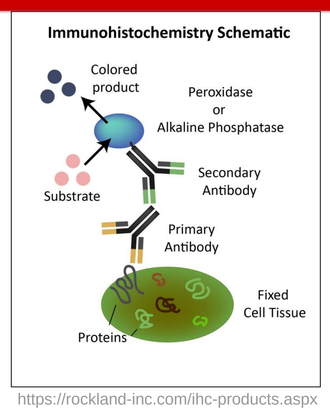
Methodology

- The first approach was to scour the internet for research papers that have conducted general gene or protein expression studies. However, this approach proved unfruitful, as the studies were too different for their data to be analyzed together. There were always modifications or manipulations of certain variables, such as inducing a certain pathway, or studying a variation of IPF.
- The second approach involved combing GEO (gene expression omnibus) for the raw data that the previously mentioned studies produced. Microarray studies provided raw data for gene expression for over 50000 genes in human IPF lung tissue vs control lung tissues. In this way, the existing studies could be compared.

IPF supplemental information



https://www.nature.com/articles/nrdp201774



https://rockland-inc.com/ihc-products.aspx

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References

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